



032301.230.SEQ.ST25.txt
SEQUENCE LISTING

<110> FARWICK, Mike, et al.

<120> NUCLEOTIDE SEQUENCES WHICH CODE FOR THE dead GENE

<130> 032301 WD 230

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 2381

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (259)..(2130)

<223>

<400> 1

caggaaaccc cgcaggggtga ctcagcatca gctgacttcg ctctcgaaac cccaaccaac
60

actgttgaag atgcaccagc atctgagggt agcgaagaga tcaccagggt tgcggatact 1
20

tctgaggacg ccgactctgc agatgcagac aacgcgagca atgtaatcaa tgagaatgag 1
80

gactcctcgg aagggtgctaa ccagccttca aacgagtcac cctctacgga agccaaatcc 2
40

ggcttcgatg cactcgga ctg cca gag cgt gta ctt gac gct gtg cgc aag 2
91

Met Pro Glu Arg Val Leu Asp Ala Val Arg Lys

1

5

10

gtg ggt tac gaa act cct tcc cca att cag gca caa acc atc cca atc 3
39

Val Gly Tyr Glu Thr Pro Ser Pro Ile Gln Ala Gln Thr Ile Pro Ile

15

20

25

ctc atg gag ggc cag gat gtt gtt ggt cta gca cag acc ggt acc ggt	3
87 Leu Met Glu Gly Gln Asp Val Val Gly Leu Ala Gln Thr Gly Thr Gly	
30 35 40	
aag act gca gct ttc gcg ctg cca atc ctt gcc cgt att gac aag tcc	4
35 Lys Thr Ala Ala Phe Ala Leu Pro Ile Leu Ala Arg Ile Asp Lys Ser	
45 50 55	
gtg cgc agc cca cag gca ctt gtg ctt gcc cct acc cgt gag cag gca	4
83 Val Arg Ser Pro Gln Ala Leu Val Leu Ala Pro Thr Arg Glu Gln Ala	
60 65 70 75	
ctt cag gtt gct gac tcc ttc caa tcc ttc gct gac cac gtc ggt ggc	5
31 Leu Gln Val Ala Asp Ser Phe Gln Ser Phe Ala Asp His Val Gly Gly	
80 85 90	
ctg aac gtt ctg cca atc tat ggt gga cag gct tac ggc att cag ctc	5
79 Leu Asn Val Leu Pro Ile Tyr Gly Gly Gln Ala Tyr Gly Ile Gln Leu	
95 100 105	
tct ggc ctg cgt cgt ggc gct cac atc gtc gtg ggt acc cca ggc cga	6
27 Ser Gly Leu Arg Arg Gly Ala His Ile Val Val Gly Thr Pro Gly Arg	
110 115 120	
atc atc gat cac ctc gaa aag ggc tcc ctg gat atc tcc gga ctg cgc	6
75 Ile Ile Asp His Leu Glu Lys Gly Ser Leu Asp Ile Ser Gly Leu Arg	

125

ttc ctc gtg ctc gat gaa gca gac gag atg ctg aac atg ggc ttc cag 7
23

Phe Leu Val Leu Asp Glu Ala Asp Glu Met Leu Asn Met Gly Phe Gln

140 145 150 155

gaa gat gtc gag cgc atc ctc gag gac acc cca gac gag aag cag gtt 7
71

Glu Asp Val Glu Arg Ile Leu Glu Asp Thr Pro Asp Glu Lys Gln Val

160 165 170

gca cta ttc tcc gca acg atg cca aac ggc att cgt cgc ctg tcc aag 8
19

Ala Leu Phe Ser Ala Thr Met Pro Asn Gly Ile Arg Arg Leu Ser Lys

175 180 185

cag tac ctg aac aac cct gct gaa atc acc gtt aag tcc gag acc agg 8
67

Gln Tyr Leu Asn Asn Pro Ala Glu Ile Thr Val Lys Ser Glu Thr Arg

190 195 200

act aac acc aac atc acc cag cgc ttc ctc aac gtt gca cac cgc aac 9
15

Thr Asn Thr Asn Ile Thr Gln Arg Phe Leu Asn Val Ala His Arg Asn

205 210 215

aag atg gat gca ctg acc cgt att ctc gag gtc acc gag ttt gaa gca 9
63

Lys Met Asp Ala Leu Thr Arg Ile Leu Glu Val Thr Glu Phe Glu Ala

220 225 230 235

atg atc atg ttc gtg cgc acc aag cac gaa act gaa gaa gtt gct gaa 10
11

Met Ile Met Phe Val Arg Thr Lys His Glu Thr Glu Glu Val Ala Glu

240	245	250	
aag ctc cgt gca cgc gga ttc tcc gca gca gcc atc aac ggc gac att 59			10
Lys Leu Arg Ala Arg Gly Phe Ser Ala Ala Ala Ile Asn Gly Asp Ile			
255	260	265	
gct cag gca cag cgt gag cgc acc gtc gac cag ctg aag gac ggc cgc 07			11
Ala Gln Ala Gln Arg Glu Arg Thr Val Asp Gln Leu Lys Asp Gly Arg			
270	275	280	
ctg gac atc ctc gtt gca acc gac gtt gca gcc cgt ggt ctt gac gtt 55			11
Leu Asp Ile Leu Val Ala Thr Asp Val Ala Ala Arg Gly Leu Asp Val			
285	290	295	
gag cgc atc tcc cac gtg ctt aac ttc gac att cca aac gac acc gag 03			12
Glu Arg Ile Ser His Val Leu Asn Phe Asp Ile Pro Asn Asp Thr Glu			
300	305	310	315
tcc tac gtt cac cgc atc ggc cgc acc ggc cgt gca gga cgt acc ggc 51			12
Ser Tyr Val His Arg Ile Gly Arg Thr Gly Arg Ala Gly Arg Thr Gly			
320	325	330	
gag gca atc ctg ttc gtg acc cca cgt gag cgt cgt atg ctt cgc tcc 99			12
Glu Ala Ile Leu Phe Val Thr Pro Arg Glu Arg Arg Met Leu Arg Ser			
335	340	345	
atc gag cgc gca acc aac gca cca ctg cac gaa atg gaa ctg cca acc 47			13

Ile Glu Arg Ala Thr Asn Ala Pro Leu His Glu Met Glu Leu Pro Thr

350

355

360

gtc gat cag gtc aac gac ttc cgc aag gtc aag ttc gct gac tcc atc 13
95

Val Asp Gln Val Asn Asp Phe Arg Lys Val Lys Phe Ala Asp Ser Ile

365

370

375

acc aag tcc ctc gag gac aag cag atg gac ctg ttc cgc acc ctg gtc 14
43

Thr Lys Ser Leu Glu Asp Lys Gln Met Asp Leu Phe Arg Thr Leu Val

380

385

390

395

aag gaa tac tcc cag gcc aac gac gtt cct cta gag gac atc gca gcg 14
91

Lys Glu Tyr Ser Gln Ala Asn Asp Val Pro Leu Glu Asp Ile Ala Ala

400

405

410

gca ctg gca acc cag gca cag tcc ggc gac ttc ctg ctc aag gag ctc 15
39

Ala Leu Ala Thr Gln Ala Gln Ser Gly Asp Phe Leu Leu Lys Glu Leu

415

420

425

cca cca gag cgc cgt gag cgc aac gac cgc cgt cgt gac cgt gac ttc 15
87

Pro Pro Glu Arg Arg Glu Arg Asn Asp Arg Arg Arg Asp Arg Asp Phe

430

435

440

gac gac cgt ggt gga cgt gga cgc gac cgt gac cgt ggc gac cgc gga 16
35

Asp Asp Arg Gly Gly Arg Gly Arg Asp Arg Asp Arg Gly Asp Arg Gly

445

450

455

gat cgt ggc tca cgc ttc gac cgc gac gac gag aac ctg gca acc tac 16

83
 Asp Arg Gly Ser Arg Phe Asp Arg Asp Asp Glu Asn Leu Ala Thr Tyr
 460 465 470 475

cgc ctc gca gtg ggc aag cgc cag cac atc cgc cca ggc gca atc gtt 17
 31
 Arg Leu Ala Val Gly Lys Arg Gln His Ile Arg Pro Gly Ala Ile Val
 480 485 490

ggc gca ctt gcc aac gaa ggt ggc ctg aac tcc aag gac ttc ggc cgc 17
 79
 Gly Ala Leu Ala Asn Glu Gly Gly Leu Asn Ser Lys Asp Phe Gly Arg
 495 500 505

atc acc atc gca gcc gac cac acc ctg gtt gaa ctg cca aag gat ctc 18
 27
 Ile Thr Ile Ala Ala Asp His Thr Leu Val Glu Leu Pro Lys Asp Leu
 510 515 520

cca cag agc gtt ctt gac aac ctg cgc gac acc cgc atc tcc ggc cag 18
 75
 Pro Gln Ser Val Leu Asp Asn Leu Arg Asp Thr Arg Ile Ser Gly Gln
 525 530 535

ctc atc aac ata gaa cgc gac tcc ggt gga cgc cca cca cgc cgc ttc 19
 23
 Leu Ile Asn Ile Glu Arg Asp Ser Gly Gly Arg Pro Pro Arg Arg Phe
 540 545 550 555

gag cgc gat gac cgt ggc gga cgc ggc gga ttc cgc ggc gac cgt gat 19
 71
 Glu Arg Asp Asp Arg Gly Gly Arg Gly Gly Phe Arg Gly Asp Arg Asp
 560 565 570

032301.230.SEQ.ST25.txt

gac cgc ggt gga cgt gga cgt gac cgt gac gat cgt gga agc cgt gga 19	20
Asp Arg Gly Gly Arg Gly Arg Asp Arg Asp Asp Arg Gly Ser Arg Gly	
575	580
	585
ggt ttc cgc ggt gga cgt gac cgt gat gat cgt ggc gga cgc ggt gga 67	20
Gly Phe Arg Gly Gly Arg Asp Arg Asp Asp Arg Gly Gly Arg Gly Gly	
590	595
	600
ttc cgc gga cgc gac gac cgc gga gac cgt ggt ggc cgt ggc ggt tac 15	21
Phe Arg Gly Arg Asp Asp Arg Gly Asp Arg Gly Gly Arg Gly Gly Tyr	
605	610
	615
cgt ggc gga cgc gac taagagttcg ttttagcttc agctcagggtt ttcgcctgag 70	21
Arg Gly Gly Arg Asp	
620	
tctggtgctt agctagaaaa atccgttget ctctctttac tgagagggca acggattttt 30	22
tctgttttct taggcttttg ttcttggggg atcttggggg aggaattcta ggaacttaga 90	22
gaagtaaag atggtgcttc gaccgcagca ccatcggttaa gattctgacc aaagaagaga 50	23
gcattgcgtt gctctctagt cagagtgcga g 81	23
<210> 2	
<211> 624	
<212> PRT	
<213> Corynebacterium glutamicum	
<400> 2	

032301.230.SEQ.ST25.txt

Met Pro Glu Arg Val Leu Asp Ala Val Arg Lys Val Gly Tyr Glu Thr
 1 5 10 15
 Pro Ser Pro Ile Gln Ala Gln Thr Ile Pro Ile Leu Met Glu Gly Gln
 20 25 30
 Asp Val Val Gly Leu Ala Gln Thr Gly Thr Gly Lys Thr Ala Ala Phe
 35 40 45
 Ala Leu Pro Ile Leu Ala Arg Ile Asp Lys Ser Val Arg Ser Pro Gln
 50 55 60
 Ala Leu Val Leu Ala Pro Thr Arg Glu Gln Ala Leu Gln Val Ala Asp
 65 70 75 80
 Ser Phe Gln Ser Phe Ala Asp His Val Gly Gly Leu Asn Val Leu Pro
 85 90 95
 Ile Tyr Gly Gly Gln Ala Tyr Gly Ile Gln Leu Ser Gly Leu Arg Arg
 100 105 110
 Gly Ala His Ile Val Val Gly Thr Pro Gly Arg Ile Ile Asp His Leu
 115 120 125
 Glu Lys Gly Ser Leu Asp Ile Ser Gly Leu Arg Phe Leu Val Leu Asp
 130 135 140
 Glu Ala Asp Glu Met Leu Asn Met Gly Phe Gln Glu Asp Val Glu Arg
 145 150 155 160
 Ile Leu Glu Asp Thr Pro Asp Glu Lys Gln Val Ala Leu Phe Ser Ala
 165 170 175
 Thr Met Pro Asn Gly Ile Arg Arg Leu Ser Lys Gln Tyr Leu Asn Asn
 180 185 190

032301.230.SEQ.ST25.txt

Pro Ala Glu Ile Thr Val Lys Ser Glu Thr Arg Thr Asn Thr Asn Ile
195 200 205

Thr Gln Arg Phe Leu Asn Val Ala His Arg Asn Lys Met Asp Ala Leu
210 215 220

Thr Arg Ile Leu Glu Val Thr Glu Phe Glu Ala Met Ile Met Phe Val
225 230 235 240

Arg Thr Lys His Glu Thr Glu Glu Val Ala Glu Lys Leu Arg Ala Arg
245 250 255

Gly Phe Ser Ala Ala Ala Ile Asn Gly Asp Ile Ala Gln Ala Gln Arg
260 265 270

Glu Arg Thr Val Asp Gln Leu Lys Asp Gly Arg Leu Asp Ile Leu Val
275 280 285

Ala Thr Asp Val Ala Ala Arg Gly Leu Asp Val Glu Arg Ile Ser His
290 295 300

Val Leu Asn Phe Asp Ile Pro Asn Asp Thr Glu Ser Tyr Val His Arg
305 310 315 320

Ile Gly Arg Thr Gly Arg Ala Gly Arg Thr Gly Glu Ala Ile Leu Phe
325 330 335

Val Thr Pro Arg Glu Arg Arg Met Leu Arg Ser Ile Glu Arg Ala Thr
340 345 350

Asn Ala Pro Leu His Glu Met Glu Leu Pro Thr Val Asp Gln Val Asn
355 360 365

Asp Phe Arg Lys Val Lys Phe Ala Asp Ser Ile Thr Lys Ser Leu Glu
370 375 380

Asp Lys Gln Met Asp Leu Phe Arg Thr Leu Val Lys Glu Tyr Ser Gln
 385 390 395 400

Ala Asn Asp Val Pro Leu Glu Asp Ile Ala Ala Ala Leu Ala Thr Gln
 405 410 415

Ala Gln Ser Gly Asp Phe Leu Leu Lys Glu Leu Pro Pro Glu Arg Arg
 420 425 430

Glu Arg Asn Asp Arg Arg Arg Asp Arg Asp Phe Asp Asp Arg Gly Gly
 435 440 445

Arg Gly Arg Asp Arg Asp Arg Gly Asp Arg Gly Asp Arg Gly Ser Arg
 450 455 460

Phe Asp Arg Asp Asp Glu Asn Leu Ala Thr Tyr Arg Leu Ala Val Gly
 465 470 475 480

Lys Arg Gln His Ile Arg Pro Gly Ala Ile Val Gly Ala Leu Ala Asn
 485 490 495

Glu Gly Gly Leu Asn Ser Lys Asp Phe Gly Arg Ile Thr Ile Ala Ala
 500 505 510

Asp His Thr Leu Val Glu Leu Pro Lys Asp Leu Pro Gln Ser Val Leu
 515 520 525

Asp Asn Leu Arg Asp Thr Arg Ile Ser Gly Gln Leu Ile Asn Ile Glu
 530 535 540

Arg Asp Ser Gly Gly Arg Pro Pro Arg Arg Phe Glu Arg Asp Asp Arg
 545 550 555 560

Gly Gly Arg Gly Gly Phe Arg Gly Asp Arg Asp Asp Arg Gly Gly Arg
 565 570 575

032301.230.SEQ.ST25.txt

Gly Arg Asp Arg Asp Asp Arg Gly Ser Arg Gly Gly Phe Arg Gly Gly
580 585 590

Arg Asp Arg Asp Asp Arg Gly Gly Arg Gly Gly Phe Arg Gly Arg Asp
595 600 605

Asp Arg Gly Asp Arg Gly Gly Arg Gly Gly Tyr Arg Gly Gly Arg Asp
610 615 620

<210> 3
<211> 28
<212> DNA
<213> Corynebacterium glutamicum

<400> 3
gatctagaaa tccggcttcg atgcactc
28

<210> 4
<211> 28
<212> DNA
<213> Corynebacterium glutamicum

<400> 4
ctaagcttcg acggttgga gttccatt
28